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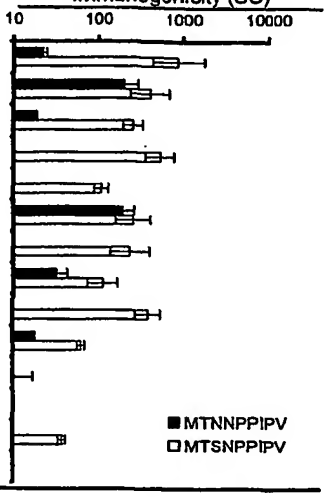
[Continued on next page]

(54) Title: METHODS OF IDENTIFYING OPTIMAL VARIANTS OF PEPTIDE EPITOPES

Amino Acid Sequence	Binding IC_{50} (nM)	# Isolates	Predicted Cross-reactivity MTNNPPIPV	Predicted Cross-reactivity MTSNPPIPV
M T S N P P I P V	52.8	60	-	+
M T N N P P I P V	128.4	33	+	+
M T S N P P V P V	21.8	26	-	+
M T G N P P I P V	125.1	15	-	+
M T G N P P V P V	2021	9	-	+
M T N N P P V P V	85.6	6	+	+
M T A N P P V P V	20.0	3	-	+
M T H N P P I P V	167.0	2	+	-
M T A N P P I P V	2.3	1	-	+
M T S D P P I P V	107.4	1	-	+
M T G N P S I P V	15.8	1	-	+
M T G N P A I P V	1200	1	-	+
M T S N P A I P V	1465	1	-	+
M T R N P P V P V	9171	1	-	-



(57) Abstract: The present invention is directed to methods for selecting a variant of a peptide epitope which induces a CTL response against another variant(s) of the peptide epitope, by determining whether the variant comprises only conserved residues, as defined herein, at non-anchor positions in comparison to the other variant(s). The present invention is also directed to variants identified by the methods above; peptides comprising such variants; nucleic acids encoding such variants and peptides; cells comprising such variants, and/or peptides, and/or nucleic acids; compositions comprising such variants, and/or peptides, and/or nucleic acids, and/or cells; as well as therapeutic and diagnostic methods for using such variants, peptides, nucleic acids, cells, and compositions.

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TR), OAPI (BF, BJ, CF, CG, CI, CM, GA, GN, GQ, GW, ML, MR, NE, SN, TD, TG).

Declarations under Rule 4.17:

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